

Table 1: Top 10 genes with the highest connectivity in the ceRNA regulatory network.

lncRNA	Degree of connectivity	miRNAs	Degree of connectivity	mRNAs	Degree of connectivity
AF131215	38	hsa-miR-17-5p	36	ASH1L	9
DIRC3	24	hsa-miR-33a-3p	30	HIPK3	9
C5orf64	21	hsa-miR-429	28	EPHA5	9
FER1L6-AS1	15	hsa-miR-20b-5p	28	NR6A1	7
AC017116	13	hsa-miR-24-3p	27	STEAP2	7
C16orf82	13	hsa-miR-761	26	SMOC1	7
TTY5	13	hsa-miR-3619-5p	25	JAZF1	7
C8orf31	12	hsa-miR-1297	24	GTF2A1	7
AC004837	11	hsa-miR-129-5p	23	NABP1	7
AC114752	10	hsa-miR-363-3p	21	FIGN	6

lncRNA, long non-coding RNA; ceRNA, competing endogenous RNA; miRNA, microRNA

Table 2: Top five terms for Biological Process (GO) of predicted mRNAs in ceRNA.

GO-term	description	Count in a gene set	False discovery rate
GO:0048583	regulation of response to stimulus	71/3882	2.53E-05
GO:0023051	regulation of signaling	65/3360	2.53E-05
GO:0010646	regulation of cell communication	65/3327	2.53E-05
GO:0009966	regulation of signal transduction	58/3033	0.00013
GO:0048518	positive regulation of biological process	84/5459	0.00070

GO, Gene Ontology; ceRNA, competing endogenous RNA

Table 3: Top 5 terms of Molecular Function (GO) of predicted mRNAs in ceRNA.

GO-term	description	Count in a gene set	False discovery rate
GO:0140110	transcription regulator activity	36/2069	0.0389
GO:0044212	transcription regulatory region DNA binding	19/829	0.0389
GO:0043167	ion binding	84/6066	0.0389
GO:0005515	protein binding	86/6605	0.0389
GO:0005488	binding	139/11878	0.0389

GO, Gene Ontology; ceRNA, competing endogenous RNA